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WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:
 - (a) a polynucleotide fragment of SEQ ID NO:1 or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No: PTA-4454, which is hybridizable to SEQ ID NO:1;
 - (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:2 or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No: PTA-4454, which is hybridizable to SEQ ID NO:1;
 - (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:2 or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No: PTA-4454, which is hybridizable to SEQ ID NO:1;
 - (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:2 or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No: PTA-4454, which is hybridizable to SEQ ID NO:1;
 - (e) a polynucleotide encoding a polypeptide of SEQ ID NO:2 or the cDNA sequence included in ATCC Deposit No: PTA-4454, which is hybridizable to SEQ ID NO:1, having tyrosine tubulin ligase activity;
 - (f) a polynucleotide which is a variant of SEQ ID NO:1;
 - (g) a polynucleotide which is an allelic variant of SEQ ID NO:1;
 - (h) an isolated polynucleotide comprising nucleotides 156 to 1775 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 541 of SEQ ID NO:2 minus the start methionine;
 - (i) an isolated polynucleotide comprising nucleotides 153 to 1775 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 541 of SEQ ID NO:2 including the start codon;
 - (j) an isolated polynucleotide comprising nucleotides 369 to 1247 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 73 to 365 of SEQ ID NO:2 including the start codon;
 - (k) an isolated polynucleotide comprising a polynucleotide that encodes at least 424 contiguous amino acids of SEQ ID NO:2;

(l) an isolated polynucleotide comprising at least 1272 contiguous nucleotides of SEQ ID NO:1;

(m) a polynucleotide which represents the complimentary sequence (antisense) of SEQ ID NO:1;

5 (n) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(m), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues;

(o) a polynucleotide comprising the BGS-42 gene;

10 (p) a polynucleotide comprising the BGS-42 promoter; and

(q) a polynucleotide comprising the nucleotide sequence provided as SEQ ID NO:27.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment consists of a nucleotide sequence encoding a human tyrosine
15 tubulin ligase.

3. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

4. A recombinant host cell comprising the vector sequences of claim 3.

5. An isolated polypeptide comprising an amino acid sequence selected
20 from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4454;

(b) a polypeptide fragment of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4454, having tyrosine tubulin ligase activity;

25 (c) a polypeptide domain of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4454;

(d) a polypeptide epitope of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4454;

30 (e) a full length protein of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4454;

(f) a polypeptide comprising amino acids 2 to 541 of SEQ ID NO:2, wherein said amino acids 2 to 541 comprising a polypeptide of SEQ ID NO:2 minus the start methionine;

(g) a polypeptide comprising amino acids 1 to 541 of SEQ ID NO:2;

5 (h) a polypeptide comprising amino acids 73 to 365 of SEQ ID NO:2; and

(i) a polypeptide comprising at least 424 contiguous amino acids of SEQ ID NO:2.

6. The isolated polypeptide of claim 5, wherein the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

7. An isolated antibody that binds specifically to the isolated polypeptide of claim 5.

8. A recombinant host cell that expresses the isolated polypeptide of claim 5.

15 9. A method of making an isolated polypeptide comprising:

(a) culturing the recombinant host cell of claim 8 under conditions such that said polypeptide is expressed; and

(b) recovering said polypeptide.

10. The polypeptide produced by claim 9.

20 11. A method for preventing, treating, or ameliorating a medical condition, comprising the step of administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 5, or a modulator thereof.

12. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

25 (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

30 13. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of claim 5 in a tyrosine tubulin ligase sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

14. An isolated nucleic acid molecule consisting of a polynucleotide having a nucleotide sequence selected from the group consisting of:

- 5 (a) a polynucleotide encoding a polypeptide of SEQ ID NO:2;
- (b) an isolated polynucleotide consisting of nucleotides 156 to 1775 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 541 of SEQ ID NO:2 minus the start codon;
- (c) an isolated polynucleotide consisting of nucleotides 369 to 1247 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 73 to 365 of SEQ ID NO:2 including the start codon;
- 10 (d) a polynucleotide encoding the BGS-42 polypeptide encoded by the cDNA clone contained in ATCC Deposit No. PTA-4454;
- (e) a polynucleotide which represents the complimentary sequence (antisense) of SEQ ID NO:1;
- 15 (f) an isolated polynucleotide consisting of a polynucleotide that encodes at least 424 contiguous amino acids of SEQ ID NO:2;
- (g) an isolated polynucleotide consisting of at least 1272 contiguous nucleotides of SEQ ID NO:1;
- 20 (h) a polynucleotide consisting of the BGS-42 gene;
- (i) a polynucleotide consisting of the BGS-42 promoter; and
- (j) a polynucleotide comprising the nucleotide sequence provided as SEQ ID NO:27.

25 15. The isolated nucleic acid molecule of claim 14, wherein the polynucleotide comprises a nucleotide sequence encoding a human tyrosine tubulin ligase.

 16. A recombinant vector comprising the isolated nucleic acid molecule of claim 15.

 17. A recombinant host cell comprising the recombinant vector of claim 16.

30 18. An isolated polypeptide consisting of an amino acid sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:2 having tyrosine tubulin ligase activity;

(b) a polypeptide domain of SEQ ID NO:2 having tyrosine tubulin ligase activity;

5 (c) a full length protein of SEQ ID NO:2;

(d) a polypeptide corresponding to amino acids 2 to 541 of SEQ ID NO:2, wherein said amino acids 2 to 541 consisting of a polypeptide of SEQ ID NO:2 minus the start methionine;

(e) a polypeptide corresponding to amino acids 1 to 541 of SEQ ID NO:2;

10 (f) a polypeptide corresponding to amino acids 73 to 365 of SEQ ID NO:2; and

(g) a polypeptide encoded by the cDNA contained in ATCC Deposit No. PTA-4454.

15 19. The method of diagnosing a pathological condition of claim 15 wherein the condition is a member of the group consisting of: a disorder related to aberrant tubulin ligase activity; a disorder related to aberrant tubulin-carboxypeptidase activity; aberrant cellular proliferation; reproductive disorders; testicular disorders; testicular cancer; pulmonary disorders; lung cancer; gastrointestinal disorders; colon cancer; stomach cancer; neural disorders; brain cancer; liver cancer; proliferative condition of the testis; proliferative condition of the lung; proliferative condition of the small intestine; proliferative condition of the brain; and proliferative condition of the lymph tissue.

20 20. The method for preventing, treating, or ameliorating a medical condition of claim 11, wherein the medical condition is selected from the group consisting of: a disorder related to aberrant tubulin ligase activity; a disorder related to aberrant tubulin-carboxypeptidase activity; aberrant cellular proliferation; reproductive disorders; testicular disorders; testicular cancer; pulmonary disorders; lung cancer; gastrointestinal disorders; colon cancer; stomach cancer; neural disorders; brain cancer; liver cancer; proliferative condition of the testis; proliferative condition of the lung; proliferative condition of the small intestine; proliferative condition of the brain; and proliferative condition of the lymph tissue.

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21. A computer for producing a three-dimensional representation of a molecule or molecular complex, wherein said molecule or molecular complex comprises the structural coordinates of the BGS-42 model provided in Figure 13 in accordance with Table IV wherein said computer comprises:

5 (a) A machine-readable data storage medium, comprising a data storage material encoded with machine readable data, wherein the data is defined by the set of structure coordinates of the model;

 (b) a working memory for storing instructions for processing said machine-readable data;

10 (c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine readable data into said three-dimensional representation; and

 (d) a display coupled to said central-processing unit for displaying said three-dimensional representation.

15 22. A method for identifying a mutant with altered biological properties, function, or activity of BGS-42 wherein said method comprises the steps of:

 (a) using a model of said polypeptide according to the structural coordinates of said model to identify amino acids to mutate; and

20 (b) mutating said amino acids to create a mutant protein with altered biological function or properties.

23. A method for designing or selecting compounds as potential modulators of BGS-42 wherein said method comprises the steps of:

 (a) identifying a structural or chemical feature of said member using the structural coordinates of said member; and

25 (b) rationally designing compounds that bind to said feature.